

#5

BATCH

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/680,121A DATE: 03/19/2001
 TIME: 10:16:17

Input Set : A:\Mueth41.app
 Output Set: N:\CRF3\03192001\I680121A.raw

3 <110> APPLICANT: French, Cynthia K.
 4 Schneider, Patrick A.
 5 Yamamoto, Karen K.
 7 <120> TITLE OF INVENTION: Prostate Cancer-Specific Marker
 9 <130> FILE REFERENCE: 107-206US-C
 11 <140> CURRENT APPLICATION NUMBER: 09/680,121A
 12 <141> CURRENT FILING DATE: 2000-10-04
 14 <150> PRIOR APPLICATION NUMBER: 60/041,246
 15 <151> PRIOR FILING DATE: 1997-03-07
 17 <150> PRIOR APPLICATION NUMBER: 60/047,811
 18 <151> PRIOR FILING DATE: 1997-05-15
 20 <150> PRIOR APPLICATION NUMBER: 09/036,315
 21 <151> PRIOR FILING DATE: 1998-03-06
 23 <150> PRIOR APPLICATION NUMBER: 09/535,597
 24 <151> PRIOR FILING DATE: 2000-03-27
 26 <160> NUMBER OF SEQ ID NOS: 27
 28 <170> SOFTWARE: PatentIn Ver. 2.1
 30 <210> SEQ ID NO: 1
 31 <211> LENGTH: 3891
 32 <212> TYPE: DNA
 33 <213> ORGANISM: Homo sapiens
 35 <220> FEATURE:
 36 <221> NAME/KEY: CDS
 37 <222> LOCATION: (151)..(1425)
 39 <220> FEATURE:
 40 <223> OTHER INFORMATION: product = Repro-PC-1.0
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 47 cagcacctcg gacagaacac gcagtaaaaa atg gct ccg atc acc acc agc cgg 174
 48 Met Ala Pro Ile Thr Thr Ser Arg
 49 1 5
 51 gaa gaa ttt gat gaa atc ccc aca gtg gtg ggg atc ttc agt gca ttt 222
 52 Glu Glu Phe Asp Glu Ile Pro Thr Val Val Gly Ile Phe Ser Ala Phe
 53 10 15 20
 55 ggc ctg gtc ttc aca gtc tct ctc ttt gca tgg atc tgc tgt cag aga 270
 56 Gly Leu Val Phe Thr Val Ser Leu Phe Ala Trp Ile Cys Cys Gln Arg
 57 25 30 .35 40
 59 aaa tca tcc aag tct aac aag act cct cca tac aag ttt gtg cat gtg 318
 60 Lys Ser Ser Lys Ser Asn Lys Thr Pro Pro Tyr Lys Phe Val His Val
 61 45 50 55
 63 ctt aag gga gtt gat att tac cct gaa aac cta aat agc aaa aag aag 366
 64 Leu Lys Gly Val Asp Ile Tyr Pro Glu Asn Leu Asn Ser Lys Lys
 65 60 65 70
 67 ttt gga gca gat gat aaa aat gaa gta aag aat aag cca gct gtg cca 414
 68 Phe Gly Ala Asp Asp Lys Asn Glu Val Lys Asn Lys Pro Ala Val Pro
 69 75 80 85

ENTERED

See p.5

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71	aag	aat	tca	ttg	cat	ctg	gat	ctt	gaa	aag	aga	gat	ctc	aat	ggc	aat	462
72	Lys	Asn	Ser	Leu	His	Leu	Asp	Leu	Glu	Lys	Arg	Asp	Leu	Asn	Gly	Asn	
73	90			95				100									
75	ttt	ccc	aaa	acc	aac	ctc	aaa	cct	ggc	agt	cct	tct	gat	ctg	gag	aat	510
76	Phe	Pro	Lys	Thr	Asn	Leu	Lys	Pro	Gly	Ser	Pro	Ser	Asp	Leu	Glu	Asn	
77	105				110				115				120				
79	gca	acc	ccg	aag	ctc	ttt	tta	gaa	ggg	gaa	aaa	gag	tca	gtt	tcc	cct	558
80	Ala	Thr	Pro	Lys	Leu	Phe	Leu	Glu	Gly	Glu	Lys	Glu	Ser	Val	Ser	Pro	
81					125				130				135				
83	gag	agt	tta	aag	tcc	agg	act	tcc	ctt	act	tca	gaa	gag	aaa	caa	gag	606
84	Glu	Ser	Leu	Lys	Ser	Ser	Thr	Ser	Leu	Thr	Ser	Glu	Glu	Lys	Gln	Glu	
85					140				145				150				
87	aag	ctg	gga	act	ctc	ttc	ttc	tcc	tta	gaa	tac	aac	ttc	gag	aga	aaa	654
88	Lys	Leu	Gly	Thr	Leu	Phe	Phe	Ser	Leu	Glu	Tyr	Asn	Phe	Glu	Arg	Lys	
89					155				160				165				
91	gca	ttt	gtg	gtc	aat	atc	aag	gaa	gcc	cgt	ggc	ttg	cca	gcc	atg	gat	702
92	Ala	Phe	Val	Val	Asn	Ile	Lys	Glu	Ala	Arg	Gly	Leu	Pro	Ala	Met	Asp	
93					170				175				180				
95	gag	cag	tgc	atg	acc	tct	gac	cca	tat	atc	aaa	atg	acg	atc	ctc	cca	750
96	Glu	Gln	Ser	Met	Thr	Ser	Asp	Pro	Tyr	Ile	Lys	Met	Thr	Ile	Leu	Pro	
97	185				190				195				200				
99	gag	aag	aag	cat	aaa	gtg	aaa	act	aga	gtg	ctg	aga	aaa	acc	ttg	gat	798
100	Glu	Lys	Lys	His	Lys	Val	Lys	Thr	Arg	Val	Leu	Arg	Lys	Thr	Leu	Asp	
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103	cca	gtc	ttt	gtt	gat	gag	acc	ttt	aca	ttc	tat	ggg	ata	ccc	tac	acc	846
104	Pro	Ala	Phe	Asp	Glu	Thr	Phe	Thr	Phe	Tyr	Gly	Ile	Pro	Tyr	Thr	Gln	
105					220				225				230				
107	atc	caa	gaa	ttg	gcc	ttt	cac	ttc	aca	att	ttg	agt	ttt	gac	agg	ttt	894
108	Ile	Gln	Glu	Leu	Ala	Leu	His	Phe	Thr	Ile	Leu	Ser	Phe	Asp	Arg	Phe	
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111	tca	aga	gat	gtt	atc	att	ggg	gaa	gtt	cta	att	cct	ctc	tcg	gga	att	942
112	Ser	Arg	Asp	Asp	Ile	Ile	Gly	Glu	Val	Leu	Ile	Pro	Leu	Ser	Gly	Ile	
113					250				255				260				
115	gaa	tta	tct	gaa	gga	aaa	atg	tta	atg	aat	aga	gag	atc	atc	aag	aga	990
116	Glu	Leu	Ser	Glu	Gly	Lys	Met	Leu	Met	Asn	Arg	Glu	Ile	Ile	Lys	Arg	
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119	aat	gtt	agg	aag	tct	tca	gga	cgg	ggg	gag	tta	ctg	atc	tct	tcg		1038
120	Asn	Val	Arg	Lys	Ser	Ser	Gly	Arg	Gly	Glu	Leu	Leu	Ile	Ser	Leu	Cys	
121					285				290				295				
123	tat	cag	tcc	acc	aca	aac	act	cta	act	gtg	gtt	gtc	tta	aaa	gct	cga	1086
124	Tyr	Gln	Ser	Thr	Asn	Thr	Ile	Leu	Thr	Val	Val	Val	Ile	Lys	Ala	Arg	
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127	cat	ctg	cct	aaa	tct	gat	gtg	tcc	gga	ctt	tca	gat	ccc	tat	gtc	aaa	1134
128	His	Leu	Pro	Lys	Ser	Asp	Val	Ser	Gly	Leu	Ser	Asp	Pro	Tyr	Val	Lys	
129					315				320				325				
131	gtg	aac	tgc	tac	cat	gcc	aaa	aag	aga	atc	tcc	aag	aag	aag	act	cat	1182
132	Val	Asn	Leu	Tyr	His	Ala	Lys	Lys	Arg	Ile	Ser	Lys	Lys	Lys	Thr	His	
133					330				335				340				
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136 Val Lys Lys Cys Thr Pro Asn Ala Val Phe Asn Glu Leu Phe Val Phe
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139 gat att cct tgt gag ggc ctt gaa gat ata agt qtt gaa ttt ttg gtt 1278
140 Asp Ile Pro Cys Glu Gly Leu Glu Asp Ile Ser Val Glu Phe Leu Val
141 365 370 375
143 ttg gat tct gaa agg ggg tcc cga aat gag gta atc ggg cag tta gtc 1326
144 Leu Asp Ser Glu Arg Gly Ser Arg Asn Glu Val Ile Gly Gln Leu Val
145 380 385 390
147 ttg ggt gca gca gca gaa gga act ggt gga gag cac tgg aaa gag atc 1374
148 Leu Gly Ala Ala Ala Glu Gly Thr Gly Gly Glu His Trp Lys Glu Ile
149 395 400 405
151 tgt gac tac ccc agg aga caa att gcc aag tgg cac gtg ctc tgt gat 1422
152 Cys Asp Tyr Pro Arg Arg Gln Ile Ala Lys Trp His Val Leu Cys Asp
153 ,410 415 420
155 ggt tagcatccta gccgtgagtt ggaacttaaa ggttttact aggcaaggag 1475
156 Gly
157 425
159 aaattttctt tctttctata ttggattgca agcttggaa atcaagctac ctttttgtg 1535
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227 gaatttgaac aggccaggag atcttaatac ctaatttcat catttctqca aaatgtacty 3575
229 ttttagaaatc tttttagaaatc tcaatgtgaa tatcttgcatt cttgttacaa atcctgcact 3635
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262 65 70 75 80
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267 Glu Lys Arg Asp Leu Asn Gly Asn Phe Pro Lys Thr Asn Leu Lys Pro
268 100 105 110
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271 115 120 125
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274 130 135 140
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277 145 150 155 160
279 Leu Glu Tyr Asn Phe Glu Arg Lys Ala Phe Val Val Asn Ile Lys Glu
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282 Ala Arg Gly Leu Pro Ala Met Asp Glu Gln Ser Met Thr Ser Asp Pro
283 180 185 190
285 Tyr Ile Lys Met Thr Ile Leu Pro Glu Lys Lys His Lys Val Lys Thr
286 195 200 205
288 Arg Val Leu Arg Lys Thr Leu Asp Pro Ala Phe Asp Glu Thr Phe Thr
289 210 215 220
291 Phe Tyr Gly Ile Pro Tyr Thr Gln Ile Gln Glu Leu Ala Leu His Phe
292 225 230 235 240
294 Thr Ile Leu Ser Phe Asp Arg Phe Ser Arg Asp Asp Ile Ile Gly Glu
295 245 250 255
297 Val Leu Ile Pro Leu Ser Gly Ile Glu Leu Ser Glu Gly Lys Met Leu
298 260 265 270

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Please Note:

Please Note: Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one 'n' or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/680,121A DATE: 03/19/2001
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L:651 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:651 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:651 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:670 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:670 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:670 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
L:686 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:686 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:686 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
L:702 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
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L:722 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15
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